

Connectivity and Adaptation of South Atlantic Coastal Fisheries Populations: A Genomic Perspective

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Coastal fisheries in the U.S. South Atlantic face mounting pressures from overfishing, habitat loss, and environmental change. To effectively manage these resources, it is essential to understand how populations are connected across geographic scales and how they adapt to environmental variability. This project applies population and seascape genomics to four model fisheries species with diverse life history strategies—white grunt (*Haemulon plumieri*), gray snapper (*Lutjanus griseus*), hogfish (*Lachnolaimus maximus*), and black grouper (*Mycteroperca bonaci*). Using thousands of genome-wide single nucleotide polymorphisms (SNPs), we will quantify neutral genetic structure, evaluate isolation by distance, estimate effective population size, and assess genetic diversity to identify potential stock boundaries, source populations, and demographic bottlenecks. In parallel, gene–environment association analyses will integrate molecular data with environmental features such as temperature, salinity, turbidity, depth, and estuarine influence to identify alleles linked to local conditions. These analyses will reveal adaptation hotspots where populations may be particularly resilient to environmental change or vulnerable to shifting oceanographic regimes. By combining genetic connectivity with signatures of adaptation, this research will provide a comparative, multi-species perspective on the evolutionary and ecological processes shaping South Atlantic coastal fisheries. The results will strengthen the scientific basis for refining management units, prioritizing conservation actions, and anticipating population responses to future environmental challenges, ultimately supporting sustainable fisheries management across the region.